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RAW SEQUENCE LISTING

DATE: 02/03/2003

PATENT APPLICATION: US/09/332,522E

TIME: 11:07:16

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\02032003\I332522E.raw

3 <110> APPLICANT: Costa, M.
 4 Doberstein, S.
 5 Elson, S.
 6 Ferguson, K.
 7 Homberger, S.
 9 <120> TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM
 AND SCREENING
 10 OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METABOLISM
 12 <130> FILE REFERENCE: 7326-101, EX99-004
 14 <140> CURRENT APPLICATION NUMBER: 09/332,522E
 15 <141> CURRENT FILING DATE: 1999-06-14
 17 <160> NUMBER OF SEQ ID NOS: 95
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 3419
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Caenorhabditis elegans
 26 <400> SEQUENCE: 1

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31	cgctcgattt	tgacatggag	cacaactggc	aagagcccgg	accatcacaa	caaccggatc	180
33	catcaattcc	cggaaatcaa	cacagtccgc	cacaggaata	ttatgatatt	gatgggtcaac	240
35	gagacgtaag	caccttacac	tccctgctca	accacaacaa	cgacgacttc	ttctcaatgc	300
37	gattttcccc	gccaaaacttt	gatctcggcg	gaggccgtgg	accttctcta	gccgccaccc	360
39	aacaattatc	tggagaaggt	cctgcaagta	tgcttaaccc	cttacaacaa	tctccaccaa	420
41	gtggaggtta	ccccccggca	gatgcctaca	gacctctatc	acttgctcaa	caactcgccg	480
43	cgccagcgat	gactccacat	caggcagcgt	cgctttttgt	taataactaat	ggaattgatc	540
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47	catatacaga	agccatggga	catatcaacg	ggtacatgtc	tccatacgac	caagctcaag	660
49	gccccatcag	accatcatat	tactcacaac	accatcaatc	tccaccacct	catcaccacc	720
51	atcaccaccc	gatgccaaaa	atccatgaga	accctgaaca	agtggcatct	ccatcgattg	780
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59	agaaggcggc	gaagattgtg	attcaggaga	cagcggaagg	ggatgaagat	gaggatgatg	1020
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63	aaaccgagcg	tcgtacggca	cacaatctca	tcgaaaagaa	gtatagatgc	tcaataaatg	1140
65	atcgaattca	acagctgaaa	gtacttttgt	gtggggatga	agctaagctt	tcaaaatcgg	1200
67	caacactacg	acgggctatt	gaacatatcg	aggagggtga	acacgagaat	caggtgttga	1260
69	agcatcatgt	tgaacaaatg	agaaaagacac	tgcagaataa	tcgattaccg	tacccggaac	1320
71	caattcaata	cactgaatac	tctgcccgat	caccgcgcga	atcatctcct	tctccacctt	1380
73	gaaatgagag	aaaacgatca	cgaatgagca	caacgactcc	tatgaagaat	ggaactagag	1440
75	atggatcttc	gaaagttacc	ctttttgcga	tgctcctagc	agttctgatt	tttaatccga	1500
77	ttggattgct	cgctggaagt	gcgatattct	caaaagccgc	tgcagaagct	ccgattgcct	1560

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79 ccccgttcga gcatggaaga gtgattgatg acccggatgg aactagcact cggacgcttt 1620
81 tctgggaagg gagtatcatc aatatgagct atgtctgggt gttcaacatc ttaatgatca 1680
83 tataatgtgg tgtcaaaactg ctgatccatg gtgaccctgt tcaagacttc atgtccgctt 1740
85 catggcagac ttttgtgacg actcgagaga aggcgagagc cgagttgaac tctggaaaatt 1800
87 tgaaaagatgc tcagagaaaag ttctgcgagt gtcttgcaac gttggatcga tgccttccat 1860
89 caccgggggt tgattcggtg ttttcggttg gctgggaatg cgttcgacat cttttgaatt 1920
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119 cacggcaaca ctattcactg atcaggaact gtccgccgaa gattttgaca gacaatctgg 2820
121 gtttggcggg tggccacgcg ttgtgtgctc gcaagatttg catagatgac cgagattccc 2880
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129 cgaaacccta ctggacacaa agcttcaagg gacaatccac gtttagtacg ctttatcaag 3120
131 aggcgtataa tcattatgcg attattaatg ggacaagggg agattgttgg agactatttg 3180
133 tctacgagct cacgtgccga atgctcaacg gagccaaccc acaagccacg tggtcaggcg 3240
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137 cggtcaaac ggacgcattt catcttcata cactggttaa actacatact tctatggatc 3360
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142 <210> SEQ ID NO: 2

143 <211> LENGTH: 1113

144 <212> TYPE: PRT

145 <213> ORGANISM: Caenorhabditis elegans

147 <220> FEATURE:

148 <221> NAME/KEY: misc feature

149 <222> LOCATION: (1073)..(1073)

150 <223> OTHER INFORMATION: "Xaa" is any amino acid

153 <400> SEQUENCE: 2

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156 1 5 10 15
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160 20 25 30
163 Pro Leu Asp Phe Asp Met Glu His Asn Trp Gln Glu Pro Gly Pro Ser
164 35 40 45
167 Gln Gln Pro Asp Pro Ser Ile Pro Gly Asn Gln His Ser Pro Pro Gln
168 50 55 60
171 Glu Tyr Tyr Asp Ile Asp Gly Gln Arg Asp Val Ser Thr Leu His Ser

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175	Leu	Leu	Asn	His	Asn	Asn	Asp	Asp	Phe	Phe	Ser	Met	Arg	Phe	Ser	Pro
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179	Pro	Asn	Phe	Asp	Leu	Gly	Gly	Gly	Arg	Gly	Pro	Ser	Leu	Ala	Ala	Thr
180				100					105					110		
183	Gln	Gln	Leu	Ser	Gly	Glu	Gly	Pro	Ala	Ser	Met	Leu	Asn	Pro	Leu	Gln
184			115					120					125			
187	Thr	Ser	Pro	Pro	Ser	Gly	Gly	Tyr	Pro	Pro	Ala	Asp	Ala	Tyr	Arg	Pro
188		130					135					140				
191	Leu	Ser	Leu	Ala	Gln	Gln	Leu	Ala	Ala	Pro	Ala	Met	Thr	Pro	His	Gln
192	145				150					155						160
195	Ala	Ala	Ser	Leu	Phe	Val	Asn	Thr	Asn	Gly	Ile	Asp	Gln	Lys	Asn	Phe
196				165						170					175	
199	Thr	His	Ala	Met	Leu	Ser	Ser	Pro	His	His	Thr	Ser	Met	Thr	Ser	Gln
200				180					185					190		
203	Pro	Tyr	Thr	Glu	Ala	Met	Gly	His	Ile	Asn	Gly	Tyr	Met	Ser	Pro	Tyr
204			195					200					205			
207	Asp	Gln	Ala	Gln	Gly	Pro	Ser	Gly	Pro	Ser	Tyr	Tyr	Ser	Gln	His	His
208		210					215						220			
211	Gln	Ser	Pro	Pro	Pro	His	His	His	His	His	His	Pro	Met	Pro	Lys	Ile
212	225				230						235					240
215	His	Glu	Asn	Pro	Glu	Gln	Val	Ala	Ser	Pro	Ser	Ile	Glu	Asp	Ala	Pro
216				245						250					255	
219	Glu	Thr	Lys	Pro	Thr	His	Leu	Val	Glu	Pro	Gln	Ser	Pro	Lys	Ser	Pro
220				260					265					270		
223	Gln	Asn	Met	Lys	Glu	Glu	Leu	Leu	Arg	Leu	Leu	Val	Asn	Met	Ser	Pro
224			275					280					285			
227	Ser	Glu	Val	Glu	Arg	Leu	Lys	Asn	Lys	Lys	Ser	Gly	Ala	Cys	Ser	Ala
228		290					295					300				
231	Thr	Asn	Gly	Pro	Ser	Arg	Ser	Lys	Glu	Lys	Ala	Ala	Lys	Ile	Val	Ile
232	305					310					315					320
235	Gln	Glu	Thr	Ala	Glu	Gly	Asp	Glu	Asp	Glu	Asp	Asp	Glu	Asp	Ser	Asp
236				325						330					335	
239	Ser	Gly	Glu	Thr	Met	Ser	Gln	Gly	Thr	Thr	Ile	Ile	Val	Arg	Arg	Pro
240				340					345					350		
243	Lys	Thr	Glu	Arg	Arg	Thr	Ala	His	Asn	Leu	Ile	Glu	Lys	Lys	Tyr	Arg
244			355					360					365			
247	Cys	Ser	Ile	Asn	Asp	Arg	Ile	Gln	Gln	Leu	Lys	Val	Leu	Leu	Cys	Gly
248		370					375					380				
251	Asp	Glu	Ala	Lys	Leu	Ser	Lys	Ser	Ala	Thr	Leu	Arg	Arg	Ala	Ile	Glu
252	385					390					395					400
255	His	Ile	Glu	Glu	Val	Glu	His	Glu	Asn	Gln	Val	Leu	Lys	His	His	Val
256				405						410					415	
259	Glu	Gln	Met	Arg	Lys	Thr	Leu	Gln	Asn	Arg	Leu	Pro	Tyr	Pro	Glu	
260				420					425					430		
263	Pro	Ile	Gln	Tyr	Thr	Glu	Tyr	Ser	Ala	Arg	Ser	Pro	Val	Glu	Ser	Ser
264			435					440					445			
267	Pro	Ser	Pro	Pro	Arg	Asn	Glu	Arg	Lys	Arg	Ser	Arg	Met	Ser	Thr	Thr
268		450					455					460				

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276                               485                               490                               495
279 Ala Gly Ser Ala Ile Phe Ser Lys Ala Ala Ala Glu Ala Pro Ile Ala
280                               500                               505                               510
283 Ser Pro Phe Glu His Gly Arg Val Ile Asp Asp Pro Asp Gly Thr Ser
284                               515                               520                               525
287 Thr Arg Thr Leu Phe Trp Glu Gly Ser Ile Ile Asn Met Ser Tyr Val
288                               530                               535                               540
291 Trp Val Phe Asn Ile Leu Met Ile Ile Tyr Val Val Val Lys Leu Leu
292 545                               550                               555                               560
295 Ile His Gly Asp Pro Val Gln Asp Phe Met Ser Val Ser Trp Gln Thr
296                               565                               570                               575
299 Phe Val Thr Thr Arg Glu Lys Ala Arg Ala Glu Leu Asn Ser Gly Asn
300                               580                               585                               590
303 Leu Lys Asp Ala Gln Arg Lys Phe Cys Glu Cys Leu Ala Thr Leu Asp
304                               595                               600                               605
307 Arg Ser Leu Pro Ser Pro Gly Val Asp Ser Val Phe Ser Val Gly Trp
308                               610                               615                               620
311 Glu Cys Val Arg His Leu Leu Asn Trp Leu Trp Ile Gly Arg Tyr Ile
312 625                               630                               635                               640
315 Ala Arg Arg Arg Arg Ser Thr Thr Lys Pro Val Ser Val Val Cys Arg
316                               645                               650                               655
319 Ser His Ala Gln Thr Ala Val Leu Tyr His Glu Ile His Gln Leu His
320                               660                               665                               670
323 Leu Met Gly Ile Thr Gly Asn Phe Glu Asp Thr Tyr Glu Pro Ser Ala
324                               675                               680                               685
327 Leu Thr Gly Leu Phe Met Ser Leu Cys Ala Val Asn Leu Ala Glu Ala
328                               690                               695                               700
331 Ala Gly Ala Ser Asn Asp Gly Leu Pro Arg Ala Val Met Ala Gln Ile
332 705                               710                               715                               720
335 Tyr Ile Ser Ala Ser Ile Gln Cys Arg Leu Ala Leu Pro Asn Leu Leu
336                               725                               730                               735
339 Ala Pro Phe Phe Ser Gly Tyr Phe Leu Arg Arg Ala Arg Arg His Val
340                               740                               745                               750
343 Arg Arg Ala Pro Glu His Ser Val Ser His Leu Leu Trp Ile Phe His
344                               755                               760                               765
347 Pro Ala Thr Arg Lys Phe Met Ser Asp Ala Lys Arg Leu Glu His Val
348                               770                               775                               780
351 Leu Ser Ser Lys Gln Lys Gln Leu Arg Phe Gly Ser Phe Val Glu Asp
352 785                               790                               795                               800
355 Glu Gln Leu Ser Pro Leu Ala Arg Ile Arg Thr Thr Leu Lys Val Tyr
356                               805                               810                               815
359 Leu Leu Ser Lys Leu Val Gln Glu Leu Val Gly Gly Asp Glu Ile Phe
360                               820                               825                               830
363 Thr Lys Asn Val Glu Arg Ile Leu Asn Asp Asn Asp Arg Leu Asp Asp
364                               835                               840                               845
367 Glu Val Asp Val Val Asp Val Ser Arg Leu Leu Val Thr Ile Ser Thr

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372 865      870      875      880
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376      885      890      895
379 His Val Leu Thr Cys Gly Ile Tyr Trp Arg Ser Asn Lys Asn Glu Leu
380      900      905      910
383 Ala Arg Gln His Tyr Ser Leu Ile Arg Asn Cys Pro Pro Lys Ile Leu
384      915      920      925
387 Thr Asp Asn Leu Gly Leu Ala Val Gly His Ala Leu Cys Ala Arg Lys
388      930      935      940
391 Ile Cys Ile Asp Asp Arg Asp Ser Pro Lys Val Ser Gln Tyr Val Cys
392 945      950      955      960
395 Ile His Thr Lys Lys Ser Leu Glu Ser Leu Arg Leu Phe Ser Thr Ser
396      965      970      975
399 Ser Arg Ala Ser Gly Val Val Ser Gly Ile Gln Glu Gly Thr Arg Arg
400      980      985      990
403 Met Ala Tyr Glu Trp Ile Met Asn Ser Leu Leu Asp Ala Trp Arg Ser
404      995      1000      1005
407 Asn Leu Phe Ala Ser Lys Pro Tyr Trp Thr Gln Ser Phe Lys Gly
408      1010      1015      1020
411 Gln Ser Thr Phe Ser Thr Leu Tyr Gln Glu Ala Tyr Asn His Tyr
412      1025      1030      1035
415 Ala Ile Ile Asn Gly Thr Arg Gly Asp Cys Trp Arg Leu Phe Val
416      1040      1045      1050
419 Tyr Glu Leu Thr Cys Arg Met Leu Asn Gly Ala Asn Pro Gln Ala
420      1055      1060      1065
W--> 423 Thr Trp Ser Gly Xaa Arg Arg Val Arg Ser Thr Lys Met Asp Ala
424      1070      1075      1080
427 Val Arg Gly Arg Val Ser Met Arg Arg Ser Ala Gln Pro Asp Ala
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436 <211> LENGTH: 1971
437 <212> TYPE: DNA
438 <213> ORGANISM: Drosophila melanogaster
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445 cgcaagtgac gtccagcaac cggaggaccc ccaactgtag aatccgcac accatcctaa 180
447 tcccaacaaa ccaatgacat cttgagacct caccagccat ggatcccttc gtgttcttca 240
449 tagtactggc atcgctttat ggcgttcttt actttttcga ccgcttcttc aagagttgca 300
451 tgcactaccc gtacgatgcc ttcttcaaga acaccgggct gagtataaat ttcattgagcc 360
453 tccactggca cactgagtgc tttaacagga ccctcctacg ctgggggatct gccggtaaca 420
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1073
Seq#:95; Xaa Pos. 70,88,99

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9